

WE CLAIM:

1. A method of soybean breeding for a yellow seed coat *Glycine max* plant having enhanced yield comprising:

- 5 (A) crossing a black seed coat *Glycine max* PI290136 parent plant or progeny thereof with a yellow seed coat *Glycine max* parent plant to produce a segregating population of progeny plants; and
- (B) screening the segregating population of progeny plants for the presence of a DNA molecular marker of a sufficient length that is homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:19-37, wherein a member of the progeny plants has an enhanced yield allele derived from the *Glycine max* PI290136 plant and that maps to linkage group U03 of the *Glycine max* PI290136 plant; and
- 10 (C) selecting the member plant for further crossing and selection, wherein the member plant selected has a yellow seed coat and enhanced yield relative to the yellow seed coat *Glycine max* parent plant.
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2. In the method of soybean breeding of claim 1, wherein Step B further comprises: screening the segregating population for the presence of a DNA molecular marker with a DNA primer pair selected from the group consisting of SEQ ID NO:1-18 primer pairs; and performing a DNA amplification method.

20 3. In the method of soybean breeding of claim 1, a DNA molecular marker of sufficient length is about 11 contiguous nucleotides homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:19-37.

4. In the method of soybean breeding of claim 1, a DNA molecular marker of sufficient length is about 18 to 24 contiguous nucleotides homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:19-37.

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5. In the method of soybean breeding of claim 1, a DNA molecular marker of sufficient length is greater than 24 contiguous nucleotides homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:19-37.

6. In the method of soybean breeding of claim 1, wherein said yellow seed coat *Glycine max* parent plant has an agronomic trait selected from the group consisting of herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance,
- 5 modified oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistance, increased digestibility, industrial enzyme production, pharmaceutical peptide and small molecule production, improved processing traits, proteins improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity,
- 10 biopolymers, and biofuel production.
7. In the method of soybean breeding of claim 1, said enhanced yield is at least 2 percent greater than the yellow seed coat *Glycine max* parent plant.
8. In the method of soybean breeding of claim 1, said enhanced yield is between 5 and 10 percent greater than the yellow seed coat *Glycine max* parent plant.
- 15 9. In the method of soybean breeding of claim 1, said enhanced yield is greater than 10 percent yield increase of the yellow seed coat *Glycine max* parent plant.
10. A method of soybean breeding comprising production of a yellow seed coat *Glycine max* plant having enhanced yield comprising:
- (A) crossing a *Glycine max* plant provided by growing a plant from the seed of
- 20 ATCC deposit #PTA-2323 or progeny thereof with an elite *Glycine max* parent plant cultivar to produce a segregating population of progeny plants; and
- (B) screening the segregating population of progeny plants for the presence of a DNA molecular marker of a sufficient length that is homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID
- 25 NO:19-37; and
- (C) identifying a member of the segregating population of progeny plants that has the DNA molecular marker that maps to linkage group U03 of the *Glycine max* plant ATCC deposit #PTA-2323; and

(D) selecting the member for further crossing and selection, wherein the member selected has a yellow seed coat and enhanced yield relative to the elite *Glycine max* parent plant cultivar.

11. In the method of soybean breeding of claim 10, wherein Step B further comprises:
 - 5 screening the segregating population of progeny plants for the presence of a DNA molecular marker with a DNA primer pair selected from the group consisting of SEQ ID NO:1-18 DNA primer pairs; and performing a DNA amplification method.
 12. In the method of soybean breeding of claim 10, a DNA molecular marker of sufficient length is about 11 contiguous nucleotides homologous or complementary to a
 - 10 DNA molecule selected from the group consisting of SEQ ID NO:19-37.
 13. In the method of soybean breeding of claim 10, a DNA molecular marker of sufficient length is about 18 to 24 contiguous nucleotides homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:19-37.
 14. In the method of soybean breeding of claim 10, a DNA molecular marker of sufficient length is greater than 24 contiguous nucleotides homologous or complementary
 - 15 to a DNA molecule selected from the group consisting of SEQ ID NO:19-37.
 15. In the method of soybean breeding of claim 10, wherein Step B comprises: screening the segregating population of progeny plants with a DNA molecular marker that is homologous or complementary to a DNA molecule selected from the group consisting of
 - 20 SEQ ID NO:19-37.
 16. In the method of soybean breeding of claim 10, said elite *Glycine max* parent plant has agronomic traits selected from the group consisting herbicide resistance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, modified oils production,
 - 25 high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistance, increased digestibility, industrial enzyme production, pharmaceutical peptides and small molecule production, improved processing traits, proteins improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity, biopolymers, and biofuel
 - 30 production.

17. In the method of soybean breeding of claim 10, said enhanced yield is at least 2 percent greater than the elite *Glycine max* parent plant.

18. In the method of soybean breeding of claim 10, said enhanced yield is between 5 and 10 percent greater than the elite *Glycine max* parent plant.

5 19. In the method of soybean breeding of claim 10, said enhanced yield is greater than 10 percent yield increase of the elite *Glycine max* parent plant.

20. A DNA molecule associated with enhanced yield homologous or complementary to a DNA molecule selected from the group consisting SEQ ID NO:21-37 located on linkage group U03 of *Glycine max* PI290136 or progeny thereof and is of a sufficient length to be
10 useful as a DNA molecular marker for an allele of a quantitative trait locus, wherein the allele provides enhanced yield in a yellow seed coat *Glycine max* plant.

21. A DNA molecule associated with an enhanced yield homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:21-37 located on linkage group U03 of a yellow seed coat *Glycine max* provided by ATCC deposit No.
15 PTA-2323 or progeny thereof and is of a sufficient length to be useful as a DNA molecular marker for an allele of a quantitative trait locus, wherein the allele provides enhanced yield in a yellow seed coat *Glycine max* plant.

22. A method of providing an isolated DNA molecule containing an allele of an enhanced yield QTL comprising:

20 (A) constructing a soybean genomic DNA library selected from the group consisting of *Glycine max* PI290136 and *Glycine max* having ATCC Accession No. PTA-2323 containing the enhanced yield QTL phenotype; and

(B) hybridizing the soybean genomic DNA library with a DNA sequence selected from the group consisting of SEQ ID NO:19-37; and

25 (C) isolating the soybean genomic DNA that hybridizes to the DNA sequence; and

(D) sequencing the isolated soybean genomic DNA containing the enhanced yield QTL and constructing a contig of sequences; and

(E) comparing the contig to a soybean genomic DNA sequence not containing the QTL; and

30 (F) identifying the polymorphisms in the contig genomic DNA; and

(G) constructing a plant transformation vector containing the soybean genomic DNA with the identified polymorphisms; and

(H) transforming plant cells with the plant transformation vector; and

(I) regenerating the plant cells into plants; and

5 (J) selecting said plants for the enhanced yield phenotype.

23. A *Glycine max* plant comprising an allele of a quantitative trait locus located on linkage group U03 associated with enhanced yield in the *Glycine max* plant, wherein said *Glycine max* plant has a yellow seed coat and wherein said allele of the quantitative trait locus is also located on linkage group U03 of a black seed coat *Glycine max* PI290136
10 plant and linked to a DNA molecular marker selected from the group consisting of SEQ ID NO:19-37.

24. A soybean seed having ATCC Accession No. PTA-2323.

25. A soybean plant or its parts produced by growing the seed of claim 24.

26. The part of the soybean plant of claim 25 comprising pollen.

15 27. The part of the soybean plant of claim 25 comprising an ovule.

28. A soybean plant of claim 25, wherein the soybean plant produces yellow seed coat seeds and is high yielding.

29. A soybean plant, or its parts, wherein at least one ancestor of the soybean plant is the soybean plant, or its parts, of claim 24.
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